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Qy	241		GAAACCTTAACTTCATCGCTTGTGGTTATTCTTCTCGGCCTGTTACCTTCATGGACAAA	300
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Qy	1501	ATGAAGCGGAGGCTCCCGATCCGAGTGGCTACTGTAGATGATAGTGCTTCTCCGATCTCA	1560
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encoding seq 4
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AB008097

LOCUS AB008097 1934 bp mRNA linear PLN 13-FEB-1999

DEFINITION Arabidopsis thaliana mRNA for cytochrome P450, complete cds.

ACCESSION AB008097

VERSION AB008097.1 GI:4176419

KEYWORDS ROTUNDIFOLIA3; cytochrome P450.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Kim, G.T., Tsukaya, H. and Uchimiya, H.

TITLE The ROTUNDIFOLIA3 gene of Arabidopsis thaliana encodes a new member
of the cytochrome P-450 family that is required for the regulated
polar elongation of leaf cells

JOURNAL Genes Dev. 12 (15), 2381-2391 (1998)

PUBMED 9694802

REFERENCE 2 (bases 1 to 1934)

AUTHORS Kim, G., Tsukaya, H. and Uchimiya, H.

TITLE Direct Submission

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Cellular Biosciences, Laboratory of Cellular Function; Bunkyo-ku,
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(E-mail: j30359@unix.cc.u-tokyo.ac.jp, Tel: +81-3-3812-2111,
Fax: +81-3-3812-2910)

FEATURES

Location/Qualifiers

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ORIGIN

Alignment Scores:

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Score:	2732.00	Matches:	524
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-507-106-4 (1-524) x AB008097 (1-1934)

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Db	111	AATTACATGGATTATTTGGTCGCTGGTTTCTTGGTTTGTACGGCCGGAATACTTCTCCGT	170
Qy	41	ProTrpLeuTrpPheArgLeuArgAsnSerLysThrLysAspGlyAspGluGluGluAsp	60
Db	171	CCATGGCTCTGGTTTCGTCTACGAAACTCGAAAACGAAAGATGGAGATGAAGAAGAAGAT	230
Qy	61	AsnGluGluLysLysLysGlyMetIleProAsnGlySerLeuGlyTrpProValIleGly	80
Db	231	AATGAGGAGAAGAAGAAGGAATGATTCCAAACGGAAGCTTAGGCTGGCCGGTGATCGGA	290
Qy	81	GluThrLeuAsnPheIleAlaCysGlyTyrSerSerArgProValThrPheMetAspLys	100
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Qy	121	SerThrAspAlaGluValAsnLysValValLeuGlnAsnHisGlyAsnThrPheValPro	140
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Qy	141	AlaTyrProLysSerIleThrGluLeuLeuGlyGluAsnSerIleLeuSerIleAsnGly	160
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Db	531	CCTCATCAAAAAAGGCTTCACACGCTCATTGGCGGTTCCCTCAGATCTCCTCACCTCAA	590
Qy	181	AspArgIleThrArgAspIleGluAlaSerValValLeuThrLeuAlaSerTrpAlaGln	200
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Qy	201	LeuProLeuValHisValGlnAspGluIleLysLysMetThrPheGluIleLeuValLys	220
Db	651	CTTCCATTGGTTCATGTTTCAGGATGAGATCAAAAAGATGACGTTTGAGATATTAGTAAAA	710
Qy	221	ValLeuMetSerThrSerProGlyGluAspMetAsnIleLeuLysLeuGluPheGluGlu	240
Db	711	GTGTTGATGAGCACATCTCCTGGTGAAGATATGAACATTCTCAAACCTGAGTTCGAAGAA	770
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Qy	281	AlaMetThrThrThrSerProAlaAsnAspValValAspValLeuLeuArgAspGlyGly	300
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Qy	321	IleProGlyGluGluThrMetProThrAlaMetThrLeuAlaValLysPheLeuSerAsp	340
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Qy	341	AsnProValAlaLeuAlaLysLeuValGluGluAsnMetGluMetLysArgArgLysLeu	360
Db	1071	AACCCCGTCGCTCTAGCCAACTCGTGGAGGAGAATATGGAGATGAAGAGGCGTAAATTG	1130
Qy	361	GluLeuGlyGluGluTyrLysTrpThrAspTyrMetSerLeuSerPheThrGlnAsnVal	380
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Qy	441	AspArgIleAsnGlySerAlaAsnSerSerIleCysPheThrProPheGlyGlyGlyGln	460
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Qy	461	ArgLeuCysProGlyLeuGluLeuSerLysLeuGluIleSerIlePheLeuHisHisLeu	480
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Db	1491	GTAACCCGGTACAGTTGGACGGCTGAGGAAGACGAGATAGTGTTCATTTCGACTGTGAAG	1550
Qy	501	MetLysArgArgLeuProIleArgValAlaThrValAspAspSerAlaSerProIleSer	520
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